SEQUENCE LISTING

<110> Behrens, Sven-Erik
Isken, Olaf
Grassmann, Claus W.
Sarisky, Robert T.

<120> A Set Of Ubiquitous Cellular Proteins
Involved in Viral Life Cycle

<130> P51375

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<141> 2005-03-11

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<151> 2003-09-12

<150> 60/410,460
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gggggcggct cctcatacca aggcaaacaa ggaggctact cacagtcgaa ctacaactcc 2580
ccggggtccg gccagaacta cagtggccct cccagctcct accagtcctc acaaggcggc 2640
tatggcagaa acgcagacca cagcatgaac taccagtaca gataa                  2685

<210> 5
<211> 702
<212> PRT
<213> Homo sapien

<400> 5
Met Arg Pro Met Arg Ile Phe Val Asn Asp Asp Arg His Val Met Ala
 1               5                  10                  15
Lys His Ser Ser Val Tyr Pro Thr Gln Glu Glu Leu Glu Ala Val Gln
            20                  25                  30
Asn Met Val Ser His Thr Glu Arg Ala Leu Lys Ala Val Ser Asp Trp
        35                  40                  45
Ile Asp Glu Gln Glu Lys Gly Ser Ser Glu Gln Ala Glu Ser Asp Asn
    50                  55                  60
Met Asp Val Pro Pro Glu Asp Asp Ser Lys Glu Gly Ala Gly Glu Gln
65                  70                  75                  80
Lys Thr Glu His Met Thr Arg Thr Leu Arg Gly Val Met Arg Val Gly
                85                  90                  95
Leu Val Ala Lys Cys Leu Leu Leu Lys Gly Asp Leu Asp Leu Glu Leu
            100                 105                 110
Val Leu Leu Cys Lys Glu Lys Pro Thr Thr Ala Leu Leu Asp Lys Val
        115                 120                 125
Ala Asp Asn Leu Ala Ile Gln Leu Ala Ala Val Thr Glu Asp Lys Tyr
    130                 135                 140
Glu Ile Leu Gln Ser Val Asp Asp Ala Ala Ile Val Ile Lys Asn Thr
145                 150                 155                 160
Lys Glu Pro Pro Leu Ser Leu Thr Ile His Leu Thr Ser Pro Val Val
                165                 170                 175
Arg Glu Glu Met Glu Lys Val Leu Ala Gly Glu Thr Leu Ser Val Asn
            180                 185                 190
Asp Pro Pro Asp Val Leu Asp Arg Gln Lys Cys Leu Ala Ala Leu Ala
        195                 200                 205
Ser Leu Arg His Ala Lys Trp Phe Gln Ala Arg Ala Asn Gly Leu Lys
    210                 215                 220
Ser Cys Val Ile Val Ile Arg Val Leu Arg Asp Leu Cys Thr Arg Val
225                 230                 235                 240
Pro Thr Trp Gly Pro Leu Arg Gly Trp Pro Leu Glu Leu Leu Cys Glu
                245                 250                 255
```

```
Lys Ser Ile Gly Thr Ala Asn Arg Pro Met Gly Ala Gly Glu Ala Leu
            260                 265                 270
Arg Arg Val Leu Glu Cys Leu Ala Ser Gly Ile Val Met Pro Asp Gly
        275                 280                 285
Ser Gly Ile Tyr Asp Pro Cys Glu Lys Glu Ala Thr Asp Ala Ile Gly
    290                 295                 300
His Leu Asp Arg Gln Gln Arg Glu Asp Ile Thr Gln Ser Ala Gln His
305                 310                 315                 320
Ala Leu Arg Leu Ala Ala Phe Gly Gln Leu His Lys Val Leu Gly Met
                325                 330                 335
Asp Pro Leu Pro Ser Lys Met Pro Lys Lys Pro Lys Asn Glu Asn Pro
            340                 345                 350
Val Asp Tyr Thr Val Gln Ile Pro Pro Ser Thr Thr Tyr Ala Ile Thr
        355                 360                 365
Pro Met Lys Arg Pro Met Glu Glu Asp Gly Glu Glu Lys Ser Pro Ser
    370                 375                 380
Lys Lys Lys Lys Lys Ile Gln Lys Lys Glu Glu Lys Ala Glu Pro Pro
385                 390                 395                 400
Gln Ala Met Asn Ala Leu Met Arg Leu Asn Gln Leu Lys Pro Gly Leu
                405                 410                 415
Gln Tyr Lys Leu Val Ser Gln Thr Gly Pro Val His Ala Pro Ile Phe
            420                 425                 430
Thr Met Ser Val Glu Val Asp Gly Asn Ser Phe Glu Ala Ser Gly Pro
        435                 440                 445
Ser Lys Lys Thr Ala Lys Leu His Val Ala Val Lys Val Leu Gln Asp
    450                 455                 460
Met Gly Leu Pro Thr Gly Ala Glu Gly Arg Asp Ser Ser Lys Gly Glu
465                 470                 475                 480
Asp Ser Ala Glu Glu Thr Glu Ala Lys Pro Ala Val Val Ala Pro Ala
                485                 490                 495
Pro Val Val Glu Ala Val Ser Thr Pro Ser Ala Ala Phe Pro Ser Asp
            500                 505                 510
Ala Thr Ala Glu Gln Gly Pro Ile Leu Thr Lys His Gly Lys Asn Pro
        515                 520                 525
Val Met Glu Leu Asn Glu Lys Arg Arg Gly Leu Lys Tyr Glu Leu Ile
    530                 535                 540
Ser Glu Thr Gly Gly Ser His Asp Lys Arg Phe Val Met Glu Val Glu
545                 550                 555                 560
Val Asp Gly Gln Lys Phe Gln Gly Ala Gly Ser Asn Lys Lys Val Ala
                565                 570                 575
Lys Ala Tyr Ala Ala Leu Ala Ala Leu Glu Lys Leu Phe Pro Asp Thr
            580                 585                 590
Pro Leu Ala Leu Asp Ala Asn Lys Lys Lys Arg Ala Pro Val Pro Val
        595                 600                 605
Arg Gly Gly Pro Lys Phe Ala Ala Lys Pro His Asn Pro Gly Phe Gly
    610                 615                 620
Met Gly Gly Pro Met His Asn Glu Val Pro Pro Pro Pro Asn Leu Arg
625                 630                 635                 640
Gly Arg Gly Arg Gly Gly Ser Ile Arg Gly Arg Gly Arg Gly Arg Gly
                645                 650                 655
Phe Gly Gly Ala Asn His Gly Gly Tyr Met Asn Ala Gly Ala Gly Tyr
            660                 665                 670
Gly Ser Tyr Gly Tyr Gly Gly Asn Ser Ala Thr Ala Gly Tyr Ser Asp
        675                 680                 685
Phe Phe Thr Asp Cys Tyr Gly Tyr His Asp Phe Gly Ser Ser
    690                 695                 700
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<210> 6
<211> 2107
<212> DNA
<213> Homo sapien

<400> 6
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gcgctcaaag ctgtgtccga ctggatagac gagcaggaaa agggtagcag cgagcaggca 180
gagtccgata acatggatgt gcccccagag gacgacagta aagaaggggc tggggaacag 240

aagacggagc acatgaccag aaccctgcgg ggagtgatgc gggtgggcct ggtggcaaag 300
tgcctcctac tcaaggggga cttggatctg gagctggtgc tgctgtgtaa ggagaagccc 360
acaaccgccc tcctggacaa ggtggccgac aacctggcca tccagcttgc tgctgtaaca 420
gaagacaagt acgaaatact gcaatctgtc gacgatgctg cgattgtgat aaaaaacaca 480
aaagagcctc cattgtccct gaccatccac ctgacatccc ctgttgtcag agaagaaatg 540
gagaaagtat tagctggaga aacgctatca gtcaacgacc ccccggacgt tctggacagg 600
cagaaatgcc ttgctgcctt ggcgtccctc cgacacgcca agtggttcca ggccagagcc 660
aacgggctga agtcttgtgt cattgtgatc cgggtcttga gggacctgtg cactcgcgtg 720
cccacctggg gtcccctccg aggctggcct ctcgagctcc tgtgtgagaa atccattggc 780
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gatgctattg ggcatctaga cagacagcaa cgggaagata tcacacagag tgcgcagcac 960
gcactgcggc tcgctgcctt cggccagctc cataaagtcc taggcatgga ccctctgcct 1020
tccaagatgc ccaagaaacc aaagaatgaa aacccagtgg actacaccgt tcagatccca 1080
ccaagcacca cctatgccat tacgcccatg aaacgcccaa tggaggagga cggggaggag 1140
aagtcgccca gcaaaaagaa gaagaagatt cagaagaaag aggagaaggc agagcccccc 1200
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aattcattcg aggcctctgg gccctccaaa aagacggcca agctgcacgt ggccgttaag 1380
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gctgtctcca cccctagtgc ggcctttccc tcagatgcca ctgccgagca ggggccgatc 1560
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ttcctag 2107

<210> 7
<211> 406
<212> PRT
<213> Homo sapien

<400> 7

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Gly Gly Pro Gly Gly Gly Phe Arg Pro Phe Val Pro His Ile Pro Phe
            20                  25                  30
Asp Phe Tyr Leu Cys Glu Met Ala Phe Pro Arg Val Lys Pro Ala Pro
        35                  40                  45
Asp Glu Thr Ser Phe Ser Glu Ala Leu Leu Lys Arg Asn Gln Asp Leu
    50                  55                  60
Ala Pro Asn Ser Ala Glu Gln Ala Ser Ile Leu Ser Leu Val Thr Lys
65                  70                  75                  80
Ile Asn Asn Val Ile Asp Asn Leu Ile Val Ala Pro Gly Thr Phe Glu
                85                  90                  95
Val Gln Ile Glu Glu Val Arg Gln Val Gly Ser Tyr Lys Lys Gly Thr
            100                 105                 110
Met Thr Thr Gly His Asn Val Ala Asp Leu Val Val Ile Leu Lys Ile
        115                 120                 125
Leu Pro Thr Leu Glu Ala Val Ala Ala Leu Gly Asn Lys Val Val Glu
    130                 135                 140
Ser Leu Arg Ala Gln Asp Pro Ser Glu Val Leu Thr Met Leu Thr Asn
145                 150                 155                 160
Glu Thr Gly Phe Glu Ile Ser Ser Ser Asp Ala Thr Val Lys Ile Leu
                165                 170                 175
Ile Thr Thr Val Pro Pro Asn Leu Arg Lys Leu Asp Pro Glu Leu His
            180                 185                 190
Leu Asp Ile Lys Val Leu Gln Ser Ala Leu Ala Ala Ile Arg His Ala
        195                 200                 205
Arg Trp Phe Glu Glu Asn Ala Ser Gln Ser Thr Val Lys Val Leu Ile
    210                 215                 220
Arg Leu Leu Lys Asp Leu Arg Ile Arg Phe Pro Gly Phe Glu Pro Leu
```

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225                 230                 235                 240
Thr Pro Trp Ile Leu Asp Leu Leu Gly His Tyr Ala Val Met Asn Asn
                245                 250                 255
Pro Thr Arg Gln Pro Leu Ala Leu Asn Val Ala Tyr Arg Arg Cys Leu
            260                 265                 270
Gln Ile Leu Ala Ala Gly Leu Phe Leu Pro Gly Ser Val Gly Ile Thr
        275                 280                 285
Asp Pro Cys Glu Ser Gly Asn Phe Arg Val His Thr Val Met Thr Leu
    290                 295                 300
Glu Gln Gln Asp Met Val Cys Tyr Thr Ala Gln Thr Leu Val Arg Ile
305                 310                 315                 320
Leu Ser His Gly Gly Phe Arg Lys Ile Leu Gly Gln Glu Gly Asp Ala
                325                 330                 335
Ser Tyr Leu Ala Ser Glu Ile Ser Thr Trp Asp Gly Val Ile Val Thr
            340                 345                 350
Pro Ser Glu Lys Ala Tyr Glu Lys Pro Pro Glu Lys Lys Glu Gly Glu
        355                 360                 365
Glu Glu Glu Glu Asn Thr Glu Arg Thr Thr Ser Arg Arg Gly Arg Arg
    370                 375                 380
Lys His Gly Asn Ser Gly Val Thr Phe Pro Ser Leu Leu Phe Leu Pro
385                 390                 395                 400
Lys Gly Lys Thr Gly Ala
                405
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<210> 8
<211> 1221
<212> DNA
<213> Homo sapien

<400> 8

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tttccccggg tcaagccagc acctgatgag acttccttca gtgaggcctt gctgaagagg 180
aaccaggacc tggctcccaa ttctgctgaa caggcatcta tcctttctct agtgacaaaa 240
ataaacaatg tgattgataa tctgattgtg gctccaggga catttgaagt gcaaattgaa 300
gaagttcgac aggtgggatc ctataaaaag gggacaatga ctacaggaca caatgtggct 360
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ccacccaatc ttcgaaaact ggatccagaa ctccatttgg atatcaaagt attgcagagt 600
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aagggaaaga ctggagccta a                                          1221
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